

SEQUENCE LISTING

<110> Ford, John
Mulero, Julio

<120> METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
POLYPEPTIDES

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<150> 09/118,205

<151> 1998-07-16

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<170> PatentIn Ver. 2.0

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aaaagtgata taataaagga accaaggaga aaattcagaa ggaaagaaaa aattgcctct 180
gcaggtgtgc gagcaggatt gcttctgcaa caaaagcctc caccagcca catcttggga 240

aaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta tcc 290
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser
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tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag 338
Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu
      20           25           30

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Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr
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ttg tat gga att atg ttt gat gca ggg agc act gga act cga att cat 434
Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His
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gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa 482
Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu
      65           70           75

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Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp
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caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc 578
Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala
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aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta 626
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cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc	866
Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile	
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acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc	914
Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly	
210 215 220	
tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca	962
Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr	
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cat agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg	1010
His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu	
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Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala	
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Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys	
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Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys	
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Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu	
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Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg	
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gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa	1298
Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys	
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Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu	
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aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc 1394
Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile
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aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta 1442
Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu
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cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg 1490
Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly
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gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tgaggccacg 1539
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cgagcttatt cttwatragg taatttactt gcmtggccgc gtttacacgt cgtgatggna 1719

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Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
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Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
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Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Glu	His	Lys	Ala	Lys	Ala	Leu	130	135	140
Leu	Phe	Glu	Val	Lys	Glu	Ile	Phe	Arg	Lys	Ser	Pro	Phe	Leu	Val	Pro	145	150	155
Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	Leu	Ala	165	170	175
Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	Arg	Gln	180	185	190
Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr	195	200	205
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Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly	245	250	255
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys	260	265	270
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	275	280	285
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	290	295	300
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	305	310	315
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	325	330	335
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	340	345	350
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	355	360	365
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr	370	375	380
Ala	Leu	Leu	Lys	Asp	Gly	Phe	Gly	Phe	Ala	Asp	Ser	Thr	Val	Leu	Gln	385	390	395

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atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg 144
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45
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Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60
tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg 240
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80
gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa 288
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95
cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa 336
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110
gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag 384
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125
gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg 432
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca	480
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Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala	
165 170 175	
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Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln	
180 185 190	
gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg	624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr	
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260 265 270	
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370 375 380

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Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

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Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
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<213> Homo sapiens

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35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

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Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	Leu	Ala	165	170	175	
Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	Arg	Gln	180	185	190	
Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr	195	200	205	
Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	Gly	Tyr	210	215	220	
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Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly	245	250	255	
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Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	290	295	300	
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	305	310	315	320
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	325	330	335	
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	340	345	350	
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	355	360	365	
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr	370	375	380	
Ala	Leu	Leu	Lys	Asp	Gly	Phe	Gly	Phe	Ala	Asp	Ser	Thr	Val	Leu	Gln	385	390	395	400
Leu	Thr	Lys	Lys	Val	Asn	Asn	Ile	Glu	Thr	Gly	Trp	Ala	Leu	Gly	Ala	405	410	415	
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 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
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 atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg 144
 Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
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 Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60
 tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg 240
 Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80
 gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa 288
 Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90 95
 cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa 336
 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110
 gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag 384
 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
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 Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
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 165 170 175

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180 185 190	
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Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr	
195 200 205	
ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc tac	672
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr	
210 215 220	
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Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His	
225 230 235 240	
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Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly	
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260 265 270	
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Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr	
275 280 285	
cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat	912
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr	
290 295 300	
gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag gag	960
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu	
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Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala	
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gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt	1056
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Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr	
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Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
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Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
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Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
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Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
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Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
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Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
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<223> Description of Artificial Sequence: primer

<400> 11

gcaggctctcc aaggaagtac g

21

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

gtgagtgtctc cctgcatcta acataattcc

30

<210> 13

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

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45

<210> 14

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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44

<210> 15

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

gcaacagcag gactacgctt actgccagaa c

31

<210> 16

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 16

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48

<210> 17

<211> 28
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<220>

<223> Description of Artificial Sequence: primer

<400> 17
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28

<210> 18
<211> 22
<212> DNA
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<220>

<223> Description of Artificial Sequence: primer

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22

<210> 19
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<212> DNA
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<220>

<223> Description of Artificial Sequence: primer

<400> 19
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24

<210> 20
<211> 29
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<223> Description of Artificial Sequence: primer

<400> 20
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29

<210> 21
<211> 29
<212> DNA
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<223> Description of Artificial Sequence: primer

<400> 21
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<210> 22
<211> 58
<212> DNA
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<400> 22
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<210> 23
<211> 58
<212> DNA
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<223> Description of Artificial Sequence: primer

<400> 23
aaccaagtct gctggttgtg atggtgatgg tgatgcgac ctctgtggga gacagcgc 58